## Sequence listing

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N GENERAL INFORMATION:
    (i) APPLICANT:
         (A) NAME: Medeva Europe Limited
         (B) STREET: 10 St James's Street
         (C) CITY: London
         (D) STATE: not applicable
         (E) COUNTRY: United Kingdom
         (F) POSTAL CODE (ZIP): SW1A 1EF
   (ii) TITLE OF INVENTION: VACCINES CONTAINING ATTENUATED BACTERIA
  (iii) NUMBER OF SEQUENCES: 4
   (iv) COMPUTER READABLE FORM:
         (A) MEDIUM TYPE: Floppy disk
         (B) COMPUTER: IBM PC compatible
         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
         (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
2) INFORMATION FOR SEQ ID NO: 1:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1287 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: DNA (genomic)
   (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Salmonella typhimurium
   (ix) FEATURE:
          (A) NAME/KEY: CDS
         (B) LOCATION:1..1281
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GCG AAT
                                                                        48
Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Meta Ile Ala Asn
 1
ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCC\GTC GTC
                                                                        96
Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
                                 25
             20
AAT AAT GGC GTC GTG CTG GAA AGC GAC GTT GAT GGC TTA ATG CAA TCA
                                                                       144
Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Het Gln Ser
                                                  45
         35
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V.	rc al	AAA Lys 50	CTC Leu	AAC Asn	GCG Ala	GGT Gly	CAG G1n 55	GCA Ala	GGT Gly	CAG G1n	CAG G1n	CTT Leu 60	CCG Pro	GAC Asp	GAC Asp	GCC Ala		192
T	cG hr 65	CTG Leu	CGT Arg	CAC His	CAG G1n	ATC Ile 70	CTG Leu	GAA G1u	CGT Arg	TTG Leu	ATT Ile 75	ATG Met	GAT Asp	CAA Gln	ATT Ile	ATC Ile 80		240
C.	TG eu	CAG G1n	ATG Met	GGT G1y	CAG G1n 85	AAG Lys	ATG Met	GGG G1y	GTG Val	AAG Lys 90	ATC Ile	ACG Thr	GAT Asp	GAG G1u	CAG G1n 95	TTG Leu		288
G.	AT sp	CAG G1n	CCA Pro	TCA Ser 100	GCC Ala	AAC Asn	ATC Ile	GCC Ala	AAA Lys 105	CAA Gln	AAC Asn	AAT Asn	ATG Met	ACG Thr 110	ATG Met	GAT Asp		336
C G	AG 1n	ATG Met	CGC Arg 115	Ser	CGT Arg	CTG Let	GCT Ala	TAC Tyr 120	GAT Asp	GGG G1 y	CTG Leu	AAC Asn	TAT Tyr 125	TCA Ser	ACC Thr	TAC Tyr		384
C A	GT .rg	AAC Asn 130	CAG G1n	ATT	CGT Arg	AAA Lys	GAG Glu 135	Met	ATT Ile	ATC Ile	TCT Ser	GAA Glu 140	GTG Val	CGC Arg	AAC Asn	AAT Asn		432
G	AG 1u 45	GTT Val	CGT Arg	CGC Arg	CGT Arg	ATC Ile 150	ACC Thr	GTT Val	TVG Leu	CCG Pro	CAA Gln 155	Glu	GTT Val	GAC <b>A</b> sp	GCG Ala	CTG Leu 160		480
G A	iCA 11 a	AAA Lys	CAG G1n	ATT	GGC Gly 165	Thr	CAA G1n	AAC Asn	GAT Asp	GC 6 Ala 170	<b>\</b> Ser	ACC Thr	GAG G1u	CTG Leu	AAC Asn 175	CTG Leu		528
S	GC er	CAT His	ATC Ile	CTG Leu 180	Ile	GCT Ala	CTG Leu	CCG Pro	GAA Glu 185	AAC Asn	CCA Pro	ACC Thr	TCC Ser	GAG Glu 190	CAG G1n	GTT Val		576
A	AC Isn	GAC Asp	GCG Ala 195	Gln	CGC Arg	CAG Gln	GCG A1 a	GAA G1u 200	Ser	ATT Ile	GTT Val	GAA G1u	GAA G1u 205	. AJ a	CGT Arg	AAC Asn		624
6	GC 61 y	GCA Ala 210	Asp	TTC Phe	GGC Gly	Lys	CTG Leu 215	Ala	ATT Ile	ACC Thr	TAC	Ser 220	Ala	GAC Asp	CAG G1n	CAG G1n		672
1	GCG 11 a 225	Leu	Lys	GGC Gly	GGT Gly	CAG Glr 230	Met	GGC Gly	TG0	GGC Gly	CGT Arg 235	Ile	CAG Gln	GAG Glu	CTG Leu	CCG Pro 240		720
(	GGG G1 y	ATT	TTC Phe	GCC Ala	CAG Glr 245	1 A1a	CTG Leu	AGC Ser	ACC Thi	GC6 A1a 250	Lys	AAA Lys	GGC Gly	GAC Asp	ATT 11e 255	GTC Val	\	768
(	GGC GT y	CCG Pro	ATI Ile	CGC Arg 260	3 Ser	GGC G13	GTC Val	GG( G1)	7T0 Phe 265	His	ATT	CTG Leu	AAA Lys	GTA Val 270	Asr	GAC Asp		816

/	CTG Leu	CGC Arg	GGT G1 y 275	CAG G1n	AGC Ser	CAG G1n	AGT Ser	ATC Ile 280	TCC Ser	GTG Val	ACC Thr	GAA G1u	GTT Val 285	CAC His	GCT Ala	CGT Arg	864
	CAC His	ATT 11e 290	CTG Leu	CTT Leu	AAG Lys	CCG Pro	TCG Ser 295	CCG Pro	ATC Ile	ATG Met	AAC Asn	GAT Asp 300	CAG G1n	CAG Gln	GCG Ala	CGC Arg	912
	CTG Leu 305	AAG Lys	CTG Leu	GAA G1u \	Glu	ATC Ile .310	GCG Ala	GCT Ala	GAC Asp	ATT Ile	AAG Lys 315	AGT Ser	GGT Gly	AAA Lys	ACC Thr	ACC Thr 320	960
	TTT Phe	GCC Ala	GCT Ala	GCG Ala	GCG A1 a 325	AAA Lys	GAG G1u	TAC Tyr	TCT Ser	CAG Gln 330	GAC Asp	CCG Pro	GGC G1 y	TCC Ser	GCT Ala 335	AAC Asn	1008
	CAG G1n	GGC G1y	GGT G1 y	GAT Asp 340	TTG Leu	GGT G1y	TGG Trp	GCT Ala	ACG Thr 345	CCA Pro	GAT Asp	ATT Ile	TTC Phe	GAC Asp 350	CCG Pro	GCG Ala	1056
	TTC Phe	CGC Arg	GAC Asp 355	GCG Ala	CTA Leu	ACG Thr	AAG Ays	CTG Leu 360	CAT His	AAA Lys	GGC Gly	CAA G1n	ATA Ile 365	Ser	GCG Ala	CCG Pro	1104
	GTA Val	CAC His 370	Ser	TCT Ser	TTC Phe	GGC Gly	TGG Trp 375	A iy H	CTG Leu	ATC Ile	GAA G1u	TTG Leu 380	Leu	GAT Asp	ACG Thr	CGT Arg	1152
	AAG Lys 385	Val	GAC Asp	AAA Lys	ACC Thr	GAT Asp 390	Αla	GCG Ala	ÇAG Gi]n	AAA Lys	GAT Asp 395	Arg	GCT Ala	TAT Tyr	CGT Arg	ATG Met 400	1200
	CTG Leu	ATG Met	AAC Asr	CGT Arg	Lys 405	Phe	TCA Ser	GAA G1u	GAA G1u	GCG Ala 410	Ala	ACC	TGG Trp	ATG Met	CAA Glr 415	GAA GTu	1248
	CAG Gln	CGC Arg	GCC Ala	ACT Thr 420	Tyr	GTT Val	AAG Lys	ATT Ile	170 Leu 425	ı Ser	AÂÇ Asn	TAA	ATGA				1287

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 427 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Asn Trp Lys Thr Leu Leu Gly Ile Ala Met Ile Ala Asn 1 5 10 15

Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser

25

Val. Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala 50 55 60

Thr Lew Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile
65 70 75 80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu 85 90 . 95

Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp 100 105 110

Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr 115 120 125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn 130 140

Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu 145 150 155 160

Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu 165 170 175

Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val 180 185 190

Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn 195 200 205

Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln 210 215

Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro 225 230 235 240

Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gy Asp Ile Val 245 250 255

Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp 260 265 270

Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg 275 280 285

His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg 290 295 300

Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr 305 310 315 320

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Phe Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn
                                    330
                325
Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro
                            360
Val His Ser\Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
                        375
    370
Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
                                     410
                405
Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn
                                 425
             420
 (2) INFORMATION FOR SEQ ID NO: 3:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1287 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: DNA (genomic)
     (vi) ORIGINAL SOURCE:
           (A) ORGANISM: E.coli
     (ix) FEATURE:
           (A) NAME/KEY: CDS
           (B) LOCATION:1..1284
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GCG AAT
                                                                         48
 Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
                             435
 ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCC GTC GTC
                                                                         96
 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
                          450
 AAT AAC GGC GTC GTG CTG GAA AGC GAC GTT GAT GGA TTA ATG CAG TCG
  Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
                                          470
                      465
  GTA AAA CTG AAC GCT GCT CAG GCA AGG CAG CAA CTT CCT GAT GAC GCG
                                                                         192
  Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
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	_				400					40E					490			
\					480					485								
•	ACG Thor	CTG Leu	CGC Arg	CAC His 495	CAA G1n	ATC Ile	ATG Met	GAA G1u	CGT Arg 500	TTG Leu	ATC Ile	ATG Met	GAT Asp	CAA G1n 505	ATC Ile	ATT Ile		240
	CTG Leu	CAG G10	ATG Met 510	GGG Gly	CAG G1n	AAA Lys	ATG Met	GGA G1 y 515	GTG Val	AAA Lys	ATC Ile	TCC Ser	GAT Asp 520	GAG G1u	CAG Gĺn	CTG Leu		288
	GAT Asp	CAG G1n 525	GGG Ala	ATT	GCT Ala	AAC Asn	ATC Ile 530	GCG Ala	AAA Lys	CAG G1n	AAC Asn	AAC Asn 535	ATG Met	ACG Thr	CTG Leu	GAT Asp		336
	CAG G1n 540	ATG Met	CGC Arg	AGC Ser	CGT	CTG Leu 545	GCT Ala	TAC Tyr	GAT Asp	GGA G1y	CTG Leu 550	AAC Asn	TAC Tyr	AAC Asn	ACC Thr	TAT Tyr 555		384
	CGT Arg	AAC Asn	CAG Gln	ATC Ile	CGC Arg 560	AAA Lys	GAG Glu	ATG Met	ATT Ile	ATC Ile 565	TCT Ser	GAA G1u	GTG Va1	CGT Arg	AAC Asn 570	AAC Asn		432
	GAG G1u	GTG Val	CGT Arg	CGT Arg 575	CGC Arg	ATC Ile	ACC Thr	ATC Ile	CTG Leu 580	CCG Pro	CAG Gln	GAA G1u	GTC Val	GAA Glu 585	TCC Ser	CTG Leu		480
	GCG Ala	CAG Gln	CAG G1n 590	Val	GGT Gly	AAC Asn	CAA Gln	AAC Ash 595	Asp	GCC Ala	AGC Ser	ACT Thr	GAG G1u 600	Leu	AAC Asn	CTG Leu		528
	AGC Ser	CAC His 605	Ile	CTG Leu	ATC Ile	CCG Pro	CTG Leu 610	Pro	GAA G1u	AAC Asn	CCG Pro	ACC Thr 615	Ser	GAT Asp	CAG G1n	GTG Va1		576
	AAC Asn 620	Glu	GCG Ala	GAA Glu	AGC Ser	CAG G1 n 625	Ala	CGC Arg	GCC Ala	ATT	GTC Val 630	Asp	CAG Gln	GCG Ala	CGT Arg	AAC Asn 635		624
)	GGC G1 y	GCT Ala	GAT Asp	TTC Phe	GGT G1 y 640	Lys	CTG Leu	GCG Ala	ATT i Ile	GCT A1a 645	His	Ser	GCC Ala	GAC Asp	CAG G1n 650	Gln		672
	GCG Ala	CTG Leu	AAC Asr	GGC GT GT S 655		CAG Gln	ATO Met	GGC Gly	TG0 Trp 660	Gly	CGT Arg	AT∏ Ile	CAG Glr	GAG G1u 665	Leu	CCC Pro		720
	GGG G1 y	ATO Ile	7TC Phe 670	e Ala	CAG Glr	GCA Ala	Le.	AGC Ser 675	Thr	GCG Ala	AAG Lys	AA/	GG0 G13 680	/ Asp	ATI Ile	GTT Val		768
	GG( G1)	CCC Pro 685	116	CG Arg	TCC Ser	GGC G13	GTT Val 690	G1	y Phe	CAT His	ATT ile	CT( E Let 69!	ı Lys	A GTT s Val	AAC Asr	GAC ASP	\	816
	сто	G CG(	C GG(	C GA	A AGO	: AA/	AA A	Γ AT	C TC	G GTG	ACC	GA	A GT	r cat	r GCT	CGC		864

1	Leu 700	Arg	G1 y	Glu	Ser	Lys 705	Asn	Ile	Ser	Val	Thr 710	Glu	Val	His	Ala	Arg 715	
\	CAT His	ATT Ile	CTG Leu	CTG Leu	AAA Lys 720	CCG Pro	TCG Ser	CCG Pro	ATC Ile	ATG Met 725	ACT Thr	GAC Asp	GAA G1u	CAG G1n	GCC A1 a 730	CGT Arg	912
	GTG Val	AAA Lys	CTG Leu	GAA G1u 735	CAG G1n	ATT Ile	GCT Ala	GCT Ala	GAT Asp 740	ATC Ile	GAG G1u	AGT Ser	GGT Gly	AAA Lys 745	ACG Thr	ACT Thr	960
	TTT Phe	GCT Ala	GCC A1\a 750	GCA Ala	ACG Thr	AAA Lys	GAG G1u	TTC Phe 755	TCT Ser	CAG G1n	GAT Asp	CCA Pro	GTC Val 760	TCT Ser	GCT Ala	AAC Asn	1008
	CAG G1n	GGC G1 y 765	GGC G1 y	GAT Asp	CTC Leu	GGC Gly	TGG Trp 770	GCT Ala	ACA Thr	CCA Pro	GAT Asp	ATT Ile 775	TTC Phe	GAT Asp	CCG Pro	GCC Ala	1056
	TTC Phe 780	CGT Arg	GAC Asp	GCC Ala	CTG Leu	ACT Thr 785	CGC Arg	CTG Leu	AAC Asn	AAA Lys	GGT G1 y 790	CAA G1n	ATG Met	AGT Ser	GCA Ala	CCG Pro 795	1104
	GTT Val	CAC His	TCT Ser	TCA Ser	TTC Phe 800	G1 y	TGG Trp	CAT His	TTA Leu	ATC Ile 805	GAA G1u	CTG Leu	CTG Leu	GAT Asp	ACC Thr 810	CGT Arg	1152
	AAT Asn	GTC Va1	GAT Asp	AAA Lys 815	Thr	GAC Asp	GĈŢ Ala	GCG Ala	CAG G1n 820	AAA Lys	GAT Asp	CGT Arg	GCA Ala	TAC Tyr 825	CGC Arg	ATG Met	1200
	CTG Leu	ATG Met	AAC Asn 830	Arg	AAG Lys	TTC Phe	TCG Ser	GAA G1u 835	<b>\</b> G1u	GCA Ala	GCA Ala	AGC Ser	TGG Trp 840	Met	CAG G1n	GAA G1u	1248
			Ala			TAC Tyr		Lys									1287

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 428 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met le Ala Asn 1 5 10 15

Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val 20 25 30

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser 35 40 45

Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala 50 \ 55 60

Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile 65 70 75 80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu 85 90 95

Asp Gln Ala Ile Alà Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp 100 105 110

Gln Met Arg Ser Arg Lèu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr 115 120 125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn 130 135 140

Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu 145 150 155 160

Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu 165 170 175

Ser His Ile Leu Ile Pro Leu Pro Glü Asn Pro Thr Ser Asp Gln Val 180 185 190

Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn 195 200 205

Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln 210 220

Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg I le Gln Glu Leu Pro 225 230 235 240

Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Ğly Asp Ile Val 245 250 255

Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp 260 265 270

Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg

His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg

Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr 305 310 315 320

Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn

8

4

325 330 335

Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala 340 345 350

Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro 355 360 365

Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg 370 375 380

Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met 385 390 395 400

Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu 405 415

Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn 420 425

C200